● /CRF Errors Corrected by the ● C Systems Branch

Serial Number: _91/090,867_

OIPE

CRF Processing Date: _6/12/98_
Edited by: _____
Verified by: _____ (STIC staff)

☐ Changed a file from non-ASCII to ASCII

☑ Changed the margins in cases where the sequence text was "wrapped" down to the next line.

☐ Edited a format error in the Current Application Data section, specifically:
_____

☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____.

ENTERED

☐ Added the mandatory heading and subheadings for "Current Application Data".

☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically:
_____

☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:
_____

☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:
_____

☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

☐ Inserted colons after headings/subheadings. Headings edited included:
_____

☐ Deleted extra, invalid, headings used by an applicant, specifically:
_____

☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as_____ .

☐ Inserted mandatory headings, specifically: _____

☐ Corrected an obvious error in the response, specifically:
_____

☐ Edited identifiers where upper case is used but lower case is required, or vice versa.

☐ Corrected an error in the Number of Sequences field, specifically:
_____

☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____

☐ Other:
_____
_____
_____

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

PAGE: 1

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION *US/09/090,867*

DATE: 06/12/98
TIME: 10:31:38

INPUT SET: S26648.raw

> **This Raw Listing contains the General Information Section and those Sequences containing ERRORS.**

```
 1                              SEQUENCE LISTING
 2
 3   (1)     General Information:
 4
 5        (i) APPLICANT: Baumgartner, James W.          Does Not Comply
 6                       Farrah, Theresa M.         Corrected Diskette Needed
 7                       Foster, Donald C.
 8                       Grant, Frank J.
 9                       O'Hara, Patrick J.
10
11       (ii) TITLE OF INVENTION: Testis-Specific Receptor
12
13      (iii) NUMBER OF SEQUENCES: 33
14
15       (iv) CORRESPONDENCE ADDRESS:
16             (A) ADDRESSEE: ZymoGenetics, Inc.
17             (B) STREET: 1201 Eastlake Avenue East
18             (C) CITY: Seattle
19             (D) STATE: WA
20             (E) COUNTRY: USA
21             (F) ZIP: 98102
22
23        (v) COMPUTER READABLE FORM:
24             (A) MEDIUM TYPE: Floppy disk
25             (B) COMPUTER: IBM PC compatible
26             (C) OPERATING SYSTEM: PC-DOS/MS-DOS
27             (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
28
29       (vi) CURRENT APPLICATION DATA:
30             (A) APPLICATION NUMBER:
31             (B) FILING DATE:
32             (C) CLASSIFICATION:
33
34     (viii) ATTORNEY/AGENT INFORMATION:
35             (A) NAME: Parker, Gary E.
36             (B) REGISTRATION NUMBER: 31,648
37             (C) REFERENCE/DOCKET NUMBER: 95-33
38
39       (ix) TELECOMMUNICATION INFORMATION:
40             (A) TELEPHONE: 206-442-6673
41             (B) TELEFAX: 206-442-6678
42
43
```

ERRORED SEQUENCES FOLLOW:

```
255    (2) INFORMATION FOR SEQ ID NO:3:
256
257        (i) SEQUENCE CHARACTERISTICS:
258            (A) LENGTH: 1167 base pairs
259            (B) TYPE: nucleic acid
260            (C) STRANDEDNESS: double
261            (D) TOPOLOGY: linear
262
263        (ii) MOLECULE TYPE: cDNA
264
265
266        (ix) FEATURE:
267            (A) NAME/KEY: CDS
268            (B) LOCATION: 10..1152
269
270
271        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
272
273    GATCCGCCC ATG GCT TTC GTT TGC TTG GCT ATC GGA TGC TTA TAT ACC      48
274              Met Ala Phe Val Cys Leu Ala Ile Gly Cys Leu Tyr Thr
275               1               5                  10
276
277    TTT CTG ATA AGC ACA ACA TTT GGC TGT ACT TCA TCT TCA GAC ACC GAG   96
278    Phe Leu Ile Ser Thr Thr Phe Gly Cys Thr Ser Ser Ser Asp Thr Glu
279        15                  20                  25
280
281    ATA AAA GTT AAC CCT CCT CAG GAT TTT GAG ATA GTG GAT CCC GGA TAC   144
282    Ile Lys Val Asn Pro Pro Gln Asp Phe Glu Ile Val Asp Pro Gly Tyr
283     30              35                  40                  45
284
285    TTA GGT TAT CTC TAT TTG CAA TGG CAA CCC CCA CTG TCT CTG GAT CAT   192
286    Leu Gly Tyr Leu Tyr Leu Gln Trp Gln Pro Pro Leu Ser Leu Asp His
287                    50                  55                  60
288
289    TTT AAG GAA TAC ACA GTG GAA TAT GAA CTA AAA TAC CGA AAC ATT GGT   240
290    Phe Lys Glu Tyr Thr Val Glu Tyr Glu Leu Lys Tyr Arg Asn Ile Gly
291                65                  70                  75
292
293    AGT GAA ACA TGG AAG ACC ATC ATT ACT AAG AAT CTA CAT TAC AAA GAT   288
294    Ser Glu Thr Trp Lys Thr Ile Ile Thr Lys Asn Leu His Tyr Lys Asp
295            80                  85                  90
296
297    GGG TTT GAT CTT AAC AAG GGC ATT GAA GCG AAG ATA CAC ACG CTT TTA   336
298    Gly Phe Asp Leu Asn Lys Gly Ile Glu Ala Lys Ile His Thr Leu Leu
299        95                  100                 105
300
301    CCA TGG CAA TGC ACA AAT GGA TCA GAA GTT CAA AGT TCC TGG GCA GAA   384
302    Pro Trp Gln Cys Thr Asn Gly Ser Glu Val Gln Ser Ser Trp Ala Glu
303    110                 115                 120                 125
304
305    ACT ACT TAT TGG ATA TCA CCA CAA GGA ATT CCA GAA ACT AAA GTT CAG   432
306    Thr Thr Tyr Trp Ile Ser Pro Gln Gly Ile Pro Glu Thr Lys Val Gln
307                    130                 135                 140
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INPUT SET: S26648.raw

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308
309    GAT ATG GAT TGC GTA TAT TAC AAT TGG CAA TAT TTA CTC TGT TCT TGG      480
310    Asp Met Asp Cys Val Tyr Tyr Asn Trp Gln Tyr Leu Leu Cys Ser Trp
311            145                 150                 155
312
313    AAA CCT GGC ATA GGT GTA CTT CTT GAT ACC AAT TAC AAC TTG TTT TAC      528
314    Lys Pro Gly Ile Gly Val Leu Leu Asp Thr Asn Tyr Asn Leu Phe Tyr
315            160                 165                 170
316
317    TGG TAT GAG GGC TTG GAT CTT GCA TTA CAG TGT GTT GAT TAC ATC AAG      576
318    Trp Tyr Glu Gly Leu Asp Leu Ala Leu Gln Cys Val Asp Tyr Ile Lys
319            175                 180                 185
320
321    GCT GAT GGA CAA AAT ATA GGA TGC AGA TTT CCC TAT TTG GAG GCA TCA      624
322    Ala Asp Gly Gln Asn Ile Gly Cys Arg Phe Pro Tyr Leu Glu Ala Ser
323    190                 195                 200                 205
324
325    GAC TAT AAA GAT TTC TAT ATT TGT GTT AAT GGA TCA TCA GAG AAC AAG      672
326    Asp Tyr Lys Asp Phe Tyr Ile Cys Val Asn Gly Ser Ser Glu Asn Lys
327            210                 215                 220
328
329    CCT ATC AGA TCC AGT TAT TTC ACT TTT CAG CTT CAA AAT ATA GTT AAA      720
330    Pro Ile Arg Ser Ser Tyr Phe Thr Phe Gln Leu Gln Asn Ile Val Lys
331            225                 230                 235
332
333    CCT TTG CCG CCA GTC TAT CTT ACT TTT ACT CGG GAG AGT TCA TGT GAA      768
334    Pro Leu Pro Pro Val Tyr Leu Thr Phe Thr Arg Glu Ser Ser Cys Glu
335            240                 245                 250
336
337    ATT AAG CTG AAA TGG GGC ATA CCT TTG GGA CCT ATT CCA GCA AGG TGT      816
338    Ile Lys Leu Lys Trp Gly Ile Pro Leu Gly Pro Ile Pro Ala Arg Cys
339            255                 260                 265
340
341    TTT GAT TAT GAA ATT GAG ATC AGA GAA GAT GAT ACT ACC TTG GTG ACT      864
342    Phe Asp Tyr Glu Ile Glu Ile Arg Glu Asp Asp Thr Thr Leu Val Thr
343    270                 275                 280                 285
344
345    GCT ACA GTT GAA AAT GAA ACA TAC ACC TTG AAA ACA ACA AAT GAA ACC      912
346    Ala Thr Val Glu Asn Glu Thr Tyr Thr Leu Lys Thr Thr Asn Glu Thr
347                290                 295                 300
348
349    CGA CAA TTA TGC TTT GTA GTA AGA AGC AAA GTG AAT ATT TAT TGC TCA      960
350    Arg Gln Leu Cys Phe Val Val Arg Ser Lys Val Asn Ile Tyr Cys Ser
351            305                 310                 315
352
353    GAT GAC GGA ATT TGG AGT GAG TGG AGT GAT AAA CAA TGC TGG GAA GGT     1008
354    Asp Asp Gly Ile Trp Ser Glu Trp Ser Asp Lys Gln Cys Trp Glu Gly
355            320                 325                 330
356
357    GAA GAC CTA TCG AAG AAA ACT TTG CTA CGT TTC TGG CTA CCA TTT GGT     1056
358    Glu Asp Leu Ser Lys Lys Thr Leu Leu Arg Phe Trp Leu Pro Phe Gly
359            335                 340                 345
360
```

INPUT SET: S26648.raw

```
361
362
363    TTC ATC TTA ATA TTA GTT ATA TTT GTA ACC GGT CTG CTT TTG CGT AAG        1104
364    Phe Ile Leu Ile Leu Val Ile Phe Val Thr Gly Leu Leu Leu Arg Lys
365    350                 355                 360                 365
366
367    CCA AAC ACC TAC CCA AAA ATG ATT CCA GAA TTT TTC TGT GAT ACA TGAAGACTTT   1159
368    1159
369    Pro Asn Thr Tyr Pro Lys Met Ile Pro Glu Phe Phe Cys Asp Thr
370                    370                 375                 380
371
-->  372    CCTCTAGA                                                              1167
373
374
```

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION   *US/09/090,867*

INPUT SET: S26648.raw

Line	Error	Original Text
258	Entered (1167) and Calc. Seq. Length (1112) differ	(A) LENGTH: 1167 base pairs
372	# of Sequences for line conflicts w/ running total	CCTCTAGA